

Docket No. CL001181DIV2
 Serial No. To Be Assigned
 Inventors: Ming-Hui WEI et al.
 Title: ISOLATED HUMAN ENZYME PROTEINS...

1 TGGAGGAGCC AGCGGAAGGA CGGTGTGCGG GCGGGCCAGC CCTGGACGAA
 51 AGAAGAGGGC CCCTCCAGGC CAGTCTGGC ACCCTGGAT AGCGGCTGCA
 101 GCCAGGCATG GCCGACTCTG CACAGGCCA GAAGCTGGTG TACCTGGTCA
 151 CAGGGGGCTG TGGCTTCTG GGAGAGCACG TGGTGCAGAAT GCTGCTGCA
 201 CGGGAGCCCG GGCTCGGGGA GCTGCGGTC TTTGACCAAC ACCTGGGTCC
 251 CTGGCTGGAG GAGCTGAAGA CAGGTACCGG GAACGTGATC GAGGCTTGTG
 301 TGCAGACCGG AACACGGTTC CTGGTCTACA CCAGCAGCAT GGAAGTTGTG
 351 GGGCTAACCA CCAAAGGTCA CCCCTCTAC AGGGGCAACG AAGACACCCC
 401 ATACGAAGCA GTGCACAGGC ACCCCCTATCC TTGCAAGAAG GCGCTGGCCG
 451 AGTGGCTGGT CCTGGAGGCC AACGGGAGGA AGGTCCGTGG GGGGCTGCCC
 501 CTGGTGACGT GTGCCCTTCG TCCCACGGC ATCTACGGTG AAGGCCACCA
 551 GATCATGAGG GACTTCTACC GCCAGGGCCT GCGCCTGGGA GTTGGCTCT
 601 TCCGGCCAT CCCGGCCTCT GTGGAGCATG GCGGGTCTA TGTGGGCAAT
 651 GTTGCCTGGA TGCACGTGCT GGCAGCCCG GAGCTGGAGC AGCGGGCAGC
 701 CCTGATGGGC GGCCAGGTAT ACTTCTGCTA CGATGGATCA CCCTACAGGA
 751 GCTACGAGGA TTCAACATG GAGTTCTGG GCGCCCTGCGG ACTGCGGCTG
 801 GTGGCGCCC GCCCATTGCT GCCCTACTGG CTGCTGGTGT TCCCTGGCTG
 851 CCTCAATGCC CTGCTGCACT GGCTGCTGCG GCAACTGGTG CTCTACGCA
 901 CCCCTGCTGAA CCCCTACACCG CTGGCCGTGG CCAACACCCAC CTTCACCGTC
 951 AGCACCGACA AGGCTCAGCG CCATTTCCGC TATGAGCCCCC TGTTCTCGT
 1001 GGAGGATAGC CGGACCCCGA CCATTCTCTG GGTACAGGCC GCTACGGGTT
 1051 CAGCCCAGTG ACGGTGGGGC TGGGGCTGG AGGGCCAGAT ACAGCACATC
 1101 CACCCAGGTC CCGAGCCCTC ACACCCCTGGA CGGGAAAGGA CAGCTGCATT
 1151 CCAGAGCAGC AGGCAGGGCT CTGGGGCCAG AATGGCTGTC CTTGTCGTAG
 1201 AGCCCTCCAC ATTTTCTTT TCTTTTTG A GACAGGGTCT TGCTCTGTCA
 1251 CCCAGACTGG AGTGCAGTG TGTGATCATA GCTCACTGCA CCCTCAACCT
 1301 CCTGGGTTCA AGCAATCCCTC CTGCCCTCAGC CTCTGAACA GCTGGGACCA
 1351 CAGGTGCACG CCACCATACC TGGCTTTTTT TTGTTGCTTT TAGAGACAGG
 1401 GTCTCACTAT ATTGCTCAAG GCTGGACTTG AACTCCCTGG CTCAAGTGT
 1451 CTTCCCACGT GGGCTCCCA AAACGCTGGA ACTACAAGTG TGAGGCCACCG
 1501 CGCCTGGCCC ACCGCCCTC CACATTTCA ATCCAGGAGC CTTGAGTCTG
 1551 TGGCTGTGTC CTGACACCTC CAGAGTTCTG AGGGCCGTCA GGACACGGGA
 1601 GGGTTTGGGG ACAGAGTGTG CTTCCCTCTG CCTATCATCA CCAGTCCTGA
 1651 TGGCCGCTTG GTGAGTGTCT GGTGCCCTGG TGGTTGCCC CAGCTCTCTT
 1701 GTGGCTTTCT GAGCAGGAAG CGAGCACTAG GCTCCACAGG CTTACGCTGT
 1751 GTCTCCTGCC AGCCACACAG CGACCCATCG GTGCAGAGTG CAGACGCGGG
 1801 TGTGGTTCCCT CAGGCCACCC TCAGCTCTC TTTGGGAGGT GATGTTCCA
 1851 TTGTGTTTCA AAGGCCCTCAC CTTCAACTGT TCTGTTTTAG AATTCCCCCTC
 1901 TGGAGGGCTA TGGCCTCCCT ATGGTTTAC CTTCCACCTA CTTCTACCTA
 1951 AGTTCCCTTCC CAGCACATCG CCAGCCCTGG GCCTGGGAT GTCCCCAATG
 2001 CTGTACCTGG CTGACCCCGG ATTAAAAGCC TCATCCACGA AAAAAAAA
 2051 AAAAAAAA AAAAAAAA A

(SEQ ID NO: 1)

FEATURES:

5'UTR: 1-107
 Start Codon: 108
 Stop Codon: 1059
 3'UTR: 1062

HOMOLOGOUS PROTEINS:

Top 10 BLAST Hits:

CRA 335001098696094 /altid=gi 11545403 /def=gb AAG37824.1 AF277...	638	0.0
CRA 335001098696092 /altid=gi 11545401 /def=gb AAG37823.1 AF277...	562	e-159
CRA 18000005106837 /altid=gi 2563999 /def=dbj BAA22931.1 (AB00...	484	e-136
CRA 18000005043125 /altid=gi 9629084 /def=ref NP_044103.1 MC15...	269	3e-71
CRA 89000000192042 /altid=gi 9634716 /def=ref NP_039008.1 ORF ...	257	2e-67
CRA 18000004899504 /altid=gi 540666 /def=pir S41971 3beta-hydri...	240	1e-62
CRA 335001098644340 /altid=gi 11251676 /def=pir T37430 hydrox...	213	2e-54
CRA 18000004942649 /altid=gi 112779 /def=sp P26670 3BHS_VACCV 3...	212	4e-54

FIGURE 1A

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CRA|18000004942648 /altid=gi|9791111 /def=ref|NP_063838.1| A44L... 211 9e-54
CRA|73000005493670 /altid=gi|9634564 /def=ref|NP_038102.1| TA55... 211 9e-54

FIGURE 1B

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EST:

gi 11283574 /dataset=dbest /taxon=96...	1283	0.0
gi 11643588 /dataset=dbest /taxon=96...	1116	0.0
gi 13134586 /dataset=dbest /taxon=960...	527	e-147
gi 9334685 /dataset=dbest /taxon=960...	462	e-128

EXPRESSION INFORMATION FOR MODULATORY USE:

gi 11283574 brain
gi 11643588 kidney
gi 13134586 colon
gi 9334685 uterus

FIGURE 1C

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1 MADSAQAQKL VYLVTTGGCGF LGEHVVRMLL QREPRLGELR VFDQHLPWL
51 EELKTGTRNV IEACVQTGTR FLVYTSSMEV VGPNTKGHPF YRGNEDTPYE
101 AVHRHPYPCS KALAEWLVLIE ANGRKVRGGL PLVTCALRPT GIYGEGHQIM
151 RDFYRQGLRL GGWLFRALPA SVEHGRVYVG NVAMHVLAA RELEQRAALM
201 GGQVYFCYDG SPYRSYEDFN MEFLGPCGLR LVGARPLLPY WLLVFLAALN
251 ALLQWLLRPL VLYAPLLNPY TLAVANTTFT VSTDKAQRHF GYEPLFSWED
301 SRTRTILWVQ AATGSAQ

(SEQ ID NO: 2)

FEATURES:

Functional domains and key regions:

[1] PDOC00001 PS00001 ASN_GLYCOSYLATION
N-glycosylation site

276-279 NTTF

[2] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

283-285 TDK

[3] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 4

1 76-79 SSME
2 97-100 TPYE
3 215-218 SYED
4 297-300 SWED

[4] PDOC00007 PS00007 TYR_PHOSPHO_SITE
Tyrosine kinase phosphorylation site

92-99 RGNEDTPY

[5] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

157-162 GLRLGG

[6] PDOC00009 PS00009 AMIDATION
Amidation site

122-125 NGRK

[7] PDOC00029 PS00029 LEUCINE_ZIPPER
Leucine zipper pattern

246-267 LAALNALLQWLLRPLVLYAPLL

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	6	26	0.633	Putative
2	237	257	1.571	Certain
3	260	280	0.819	Putative

FIGURE 2A

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BLAST Alignment to Top Hit:

>CRA|335001098696094 /altid=gi|11545403
 /def=gb|AAG37824.1|AF277719_1 (AF277719) 3
 beta-hydroxy-delta 5-C27-steroid oxidoreductase [Homo
 sapiens] /org=Homo sapiens /taxon=9606 /dataset=nraa
 /length=369
 Length = 369

Score = 638 bits (1627), Expect = 0.0
 Identities = 315/369 (85%), Positives = 316/369 (85%), Gaps = 52/369 (14%)

Query: 1 MADSAQAQKLVLYVTGGCGFLGEHVRMILLQREPRLGELRVFDQHLPWLEELKTG---- 56
 MADSAQAQKLVLYVTGGCGFLGEHVRMILLQREPRLGELRVFDQHLPWLEELKTG
 Sbjct: 1 MADSAQAQKLVLYVTGGCGFLGEHVRMILLQREPRLGELRVFDQHLPWLEELKTGPVRV 60

Query: 57 -----TRNVIEACVQTG 68
 TRNVIEACVQTG
 Sbjct: 61 TAIQGDVTQAHEVAAVAGAHVVIHTAGLVDVFGRASPKTIHEVNQGTRNVIEACVQTG 120

Query: 69 TRFLVYTSSMEVVGPNKGHPFYRGNEDETPYEAVHRHPYPCSKALAELVWLEANGRKVRG 128
 TRFLVYTSSMEVVGPNKGHPFYRGNEDETPYEAVHRHPYPCSKALAELVWLEANGRKVRG
 Sbjct: 121 TRFLVYTSSMEVVGPNKGHPFYRGNEDETPYEAVHRHPYPCSKALAELVWLEANGRKVRG 180

Query: 129 GLPLVTCALRPTGIYGEHQIMRDFYRQGLRLGGWLFRAPASVEHGRVYVGNVAWMHVL 188
 GLPLVTCALRPTGIYGEHQIMRDFYRQGLRLGGWLFRAPASVEHGRVYVGNVAWMHVL
 Sbjct: 181 GLPLVTCALRPTGIYGEHQIMRDFYRQGLRLGGWLFRAPASVEHGRVYVGNVAWMHVL 240

Query: 189 AARELEQRAALMGGQVYFCYDGSPYRSYEDFNMEFLGPCGLRLVGARPLLPYWLLVFLAA 248
 AARELEQRAALMGGQVYFCYDGSP+RSYEDFNMEFLGPCGLRLVGARPLLPYWLLVFLAA
 Sbjct: 241 AARELEQRAALMGGQVYFCYDGSPHRSYEDFNMEFLGPCGLRLVGARPLLPYWLLVFLAA 300

Query: 249 LNALLQWLLRPLVLYAPLLNPYTLAVANTTFTVSTDKAQRHFGYEPLFSWEDSRTRTILW 308
 LNALLQWLLRPLVLYAPLLNPYTLAVAN TFTVSTDKAQRHFGYEPLFSWEDSRTRTILW
 Sbjct: 301 LNALLQWLLRPLVLYAPLLNPYTLAVANATFTVSTDKAQRHFGYEPLFSWEDSRTRTILW 360

Query: 309 VQAATGSAQ 317
 VQAATGSAQ
 Sbjct: 361 VQAATGSAQ 369 (SEQ ID NO: 4)

Hmmr search results (Pfam):

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
PF01073	3-beta hydroxysteroid dehydrogenase/isomeras	558.2	5.5e-164	2
PF01370	NAD dependent epimerase/dehydratase family	13.3	0.005	1
PF00438	S-adenosylmethionine synthetase	1.8	0.78	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
PF01370	1/1	12	31	..	1	20	[.] 13.3 0.005
PF01073	1/2	1	52	[.]	1	53	[.] 69.6 3.9e-18
PF00438	1/1	289	299	..	365	376	[.] 1.8 0.78
PF01073	2/2	55	313	..	159	425	[.] 489.6 2.4e-143

FIGURE 2B

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1 ATTTGCATTA GCCGGTGGCA GCCAACAGGT GCCTGTTTG GAGAGAGGTC
51 CAGGGAGGAG AGATGAGCAG GGTGCCGTTG GTGACATGGC CAGTCATTTC
101 AGGAGCTGCC CCAACCCAG ACTGCCCA GCAGTCGGG ACCCCACTGT
151 GACCAGGCAAG ATGCTCGAAG GAGTCAGTGG CTCTCTTAC CAGTCAGAT
201 TTCCCTGGAG TTCCCTGGG GTGACTTAGA ATGGCCACCA GAGGCTTAGG
251 ATGCTGCCCA AAAGAGGGAG GGCTCTGGA AGCAGAGTCG AGAGAGTCAG
301 TGCCGGGTTA GCGGGAGCTG GAGGAGAGC TGCACTCCA GGCGTGGTGG
351 GCGTGGACCT GGGGTGCTGG CTGGCAGGCG TGCTCAGGGG CAGGAAGTGG
401 GGGACTCTTC CCTGACCATC GCATCTCACC CTGGCAGATG GTGGCCGACA
451 TGCAGGGAGAA GCGCTACGTG CAGGAGGGCA TTGGCAGCAG CTACCTGTT
501 CGGGTGGACCC ACGACACCAT CATCGATGCC ACCAAGTGTG GCAACCTGGC
551 CAGATTCACT AACCACTGCT GCACGGTGC CGAGGGGCCA GCGGGGCGAG
601 GAGTTGGGGG TCGGTGGGGG TGCCACGGC TCACACGCC TTCCATCCGC
651 AGCCTAACTG CTACGCCAAG GTCATCACC TCGAGTCCC GAAGAAGATC
701 GTGATCTACT CCAAGCAGCC CATTGGCGTG GACGAGGAGA TCACCTACGA
751 CTACAAGTTC CCACTGGAAG ACAACAAGAT CCCGTGTCTG TGTGGCACAG
801 AGAGCTGCCG GGGCTCCCTA AACTGAGGTG GGGCAGGATG GGTGCCAC
851 CCCCTATTAA TTCCCCCTGG TGCCCTGAGC TCCCAGCACC CCCCCAGCCT
901 TAGTGGGCTC AGCAGGGCCC ACATGCCCACTCCTCAAGC GTGGGGTTGG
951 GGGCCCAAG CCCAGCGAGG GAGCCTCAGT CCCGGAGGC AGCTTCTGCC
1001 TCTCCTGTCG CCCCTGCCCA CCACCCCCCTG ATTGTTTTTC TTTGCGGAGA
1051 AGAAGCTGTA AATGTTTTGT AGCAGCCAGC AGCTGTTTCC TGTGAAAC
1101 TGGGGTGCCTG GCCTGTACAG ATTCTGTCTT GGGGGCTAC ACAGTCTCT
1151 CGCTTGTGT TAATGGGAC TTCCCCCTAAC GCGCTGCGT TACCCCTCCC
1201 CAGTTAGGG GTCTCTGGGG CAGTGGCCAT GTTCTCCCCC TGGGGGGCT
1251 CTGCACCCCCC AGTCCTGGGG ACTCGTGCCT TGAAACCTG CTCATCTGT
1301 TCCTGCCAGA CCCTGAGGGT CACCCCTCCA CCCTGGTGTC ACTCCCCGGC
1351 TCAGGCCAGGC CAGGATGGCG GGGTGGGTCC CTTTGCTGG GCTGACTGT
1401 ACATATGTTA ATAGCGAAA CCCGACGCCA CATTGTTATA ATTGTGATTA
1451 AACTTTATTG TACAAAAGTG TTGGTGGCGT GTATTTGGC AGGAGCGAGG
1501 GTTGGGGGGT AGAGGGCAGC GAGGGTTGTG CAAGTTGAAG AGAGGGAAA
1551 GTGGGTACCT GAAGTGTGGG GCAGGTAAAG GGGCCTTCAG GCAAGAGCCC
1601 AGACCTGCAG AGACAGTCCG AGACTGTCTC GGACCCCCCTG ACAGGCTGCA
1651 GCAGCCGCAC CCGCACCGG AATACCCAC CAGTCCCCCG CAGGGTGGT
1701 CCAAGGTCAAG GCCTCCCCCTT CCTACAATCA CAGCTGCAGC TGGACCTCCG
1751 GCCTCCTGGG AAGCCCAGCA GGAGGGAGG CCTGAGGTCA CACTGTGGG
1801 TGAGGTCAAC GCTGGCTCCA CCCACAGGCC CAGACCCCCCTT CAGCCCACTC
1851 TGCAAGTTCG AGCTTCATCC CCACCAAGTT CTCCGCTGGA CCCAGATGCC
1901 AGTGGAGCAC AGAGGCCCG CCAGGGGGCG CTTGGGGCA AGACTGGTGG
1951 GGGTTGTGGC TGGGCGGGT TCTGTTCTG GAATGGGGCA GGAGGGAGAA
2001 GGAGGAGGCC CGGGAGGAGC GGTGTGGCGG CCGGCCAGCC CTGGACGAAA
2051 GAAGAGGGCC CCTCCAGGCC AGTCTGGCA CCGTGGGATA CGGGCTGCA
2101 GTAGGCAGAG CGCTGCCAG TGCGCAGGTG GCCTTCCCT CCATCCGGCC
2151 CTTCCACCT TCCCTATAACC TTCCCCCTCAC CTCCCTCAAC TCCGGCCTC
2201 CCCACCCCTT TACTGCTTCA AAATCTCTC CCCTAAACCC TGACCCCTTC
2251 CTGCACCCCCA AGCCGCCCTC TCTCTCCGTA ACTCAGCCAT CAGCAGGGC
2301 AGACGGCAGG TGGCCTGGTT GCTGCAGCTC CCAGGATCAG CTCTGCCCTC
2351 CCGCCAAACG CCAGCTCGT CACCGCTCCA GGGCACCTCC AGCACTAAC
2401 GGTGGTTGCA GCAGGTGGCA GCCAGCCCCCT GGATGAGCCA AGGTCTCTC
2451 CCCAGCCAGG CATGGCCGAC TCTGCACAGG CCCAGAAGCT GGTGTACCTG
2501 GTCACAGGGG GCTGTGGCTT CCTGGGAGAG CACGTGGTGC GAATGCTGCT
2551 GCAGCGGGAG CCCCGCTCG GGGAGCTGC GGTCTTTGAC CAACACCTGG
2601 GTCCCTGGCT GGAGGAGCTG AAGACAGGTT CTTGTTGGGG GAGCTGTGG
2651 TGGAGAGGGT GTGGACGCTT CCCCCAACCT TCCCAAGCTG GGATCCCCAC
2701 CCCTGCAGTG GAACAGATGA TGCTGGTTTC TGTCACATG GATGGGTGCA
2751 GTGAGTCACA TTGGGAACGT GACTCCAGGG TGGAAGATGA ACCCAGCCTC
2801 TGGCCTCTGG CCCCAGCTCT GACATGGCCT GTGTCTCCA ACCCCGGCA
2851 GGGCCTGTGA GGGTGACTGC CATCCAGGGG GACGTGACCC AGGCCATG
2901 GGTGGCAGCA GCTGTGGCCG GAGCCCATGT GGTCACTCCAC ACGGCTGGC
2951 TGGTAGACGT GTGGCAGG GCCAGTCCC AGACCATCCA TGAGGTCAAC
3001 GTGCAGGGTG AGGAGCTCTG GACACTCTG GCCACTTGC CTGTTGTT
3051 CCCACTCTGT CTTGGCCTT GACCTCCGGT GACTCCCCCTG GGACAAGTTG

FIGURE 3A

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3101 TCCTATTGAC AGCCCTGCC 2500 CGCCCTCCCC TGACCTGTCA TGTTTTCCC
3151 TGGACCTGGG ATGGGGAGGA GGAAGATGCA GAGAGGGAAG AAGCTGCAGC
3201 TTGGATACGC CTCCTCTCT GCAGGTACCGA CGGAACGTGA TCGAGGCTTG
3251 TGTGCAGACG GGAACACCGT TCCGGTCTA CACCAAGGTG ATGGAAGTTG
3301 TGGGGCTAA CACCAAAGGT CACCCCTCT ACAGGTGAGT GGCAGGCCCT
3351 CTTGTCTCT AAGAGCCCAT TTCCCTCAGC ATTGAGTCTT CCTTCTCCTC
3401 CCACCAGGGG CAACGAAGAC ACCCCATACG AAGCAGTGCA CAGGCACCCC
3451 TATCCTTGCA GCAAGGCCCT GGGCGAGTGG CTGGTCTTGG AGGCCAACGG
3501 GAGGAAGGTG AGCCCAAGAA AAGGAGGCGC AGAGATGGGG CTCCCTGCCCT
3551 GCACACCCCC TTACCCCTGCC AGCCCAAGGA GGCCGGGCC GAGAGCAAGC
3601 TGTGGGTCTC CAGGTCTCAG CAGTACCTGC CTTCGCCCCC AGGTCCGTGG
3651 GGGGCTGCCCT CTGGTACGT GTGCCCTTCG TCCCACGGGC ATCTACGGTG
3701 AAGGCCACCA GATCATGAGG GACTTCTACC GCCAGGCCCT GCGCTGGGA
3751 GTTGGGTCTC TCCGGCCAT CCCGGCTCT GTGGAGCATG GCCGGGTCTA
3801 TGTGGGTGAG GACTGGCTA GGCAGGGGAA GGCTGAGAAT ATGGCAGGAG
3851 GACTTGTCT AGAAGGGGGC AGGACCCACA TGGCCCTGGG AGAGAAGTGT
3901 GGACTCTGGC TAGAAAAATA TGGTCTATAC ATGGGCAAG GTAGACTGTG
3951 ATTATGTCTC CACAGCCTGC AGAGAATACA GGATCCATGC AAGTTGGGAC
4001 ATTAAAAAGT GTATCATAGG CTACAGAGAA GATTGCAAGT ATGGGAGCAG
4051 CCATCCCCCA GGAGAGGGAGA GGAGAGGGAC AGTGTGTACA CAGCACTAAA
4101 AGGGCTGGGT TCAGTGGCTC GCATCTATAA TCCCGACACT TTAGGAGGGCT
4151 GAGGCGGGAG GATGGCTGA GCCCAGGAGT TGGAGGCTGC AGTGAAGCTAT
4201 GACCGCACCA CTGCACTCCA GCCTGGATGA CAGAGACAGA CCCTGTCTCT
4251 AAAACTTTT TTAAAGGAAG TAGCATCTAC ACAGGGATA AGTCACCTG
4301 CCACCTCATC CTGCAGTCCC CAAGCCTCTC AGGGCCACC ACGCAGGTCC
4351 TGGTTCTCTC ATCCTCTCCC CAGGTTCTT GCAGATGCA GCTGGCCAG
4401 GAGAGCAAGT GACTACCAGG GCGAGGGAGA AGGCAAGCTT TCCCAGGCTG
4451 CTGTGGGGAT GTGGGCCGCA ACTACCTGGG CCGAACAGAGG GGGTGGCCCA
4501 GGAGAGCAGC CTCGATGTGG TGTGCAAGG GCACTCAGGG GTGTGTCGC
4551 CTCTCTTCCG CCACCGGCAG GCAATGTTGC CTGGATGCAC GTGCTGGCAG
4601 CCCGGGAGCT GGAGCAGCGG GCAGCCCTGA TGGGCGGCCA GGTATAACTTC
4651 TGCTACGATG GATCACCTCA CAGGAGCTAC GAGGATTTCACATGGAGTT
4701 CCTGGGCCCCC TGCGGACTGC GGCTGGTGGG CGCCCGCCCA TTGCTGCCCT
4751 ACTGGCTGCT GGTGTTCTG GCTGCCCCCTCA ATGCCCCCTGC GCAGTGGCTG
4801 CTGCGGCCAC TGGTGCCTA CGCACCCCTG CTGAACCCCT ACACGCTGGC
4851 CGTGGCAAC ACCACCTTCA CGTCAGCAC CGACAAGGCT CAGGCCATT
4901 TCGGCTATGA GCCCCCTGTC TCGTGGGAGG ATAGCCGAC CCGCACCAATT
4951 CTCTGGGTAC AGGCCGCTAC GGGTTTCAGCC CAGTGAAGGT GGGGCTGGGG
5001 CCTGGAGGCC CAGATACAGC ACATCCACCC AGTCCCCAG CCCTCACACC
5051 CTGGACGGGA AGGGACAGCT GCATTCAGA GCAAGGAGCA GGGCTCTGG
5101 GGGCAGAATG GCTGCTTTC TCGTAGAGCC CTCCACATTT TCTTTTTCTT
5151 TTTTGAGACA GGGTCTGCT CTGTCACCCA GACTGGAGTG CAGTGGTGTG
5201 ATCATAGCTC ACTGCACCCCT CAACCTCTG GGTCAAGCA ATCCTCTGC
5251 CTCAGCTCC TTGAACAGCT GGGACACAG GTGCACGCCA CCACACCTGG
5301 TTTTTTTTGT TTGTTTTAG AGACAGGGTC TCACTATATT GCTCAGGCTG
5351 GTCTGAACCT CCTGGCTCA AGTGTGAG CCACCGCGCC TGGCCCAAGC CCTCCACATT
5401 GCTGGAACTA CAAAGTGTGAG CCACCGCGCC TGGCCCAAGC CCTCCACATT
5451 TTCAATCCAG GAGCCTTGAG TCTGTGTTGT GTCCTGACAC CTCCAAGTT
5501 TAGGGCGTC AGGACACGGG AGGGTTTGGG GACAGAGTGT CCTTCTCTG
5551 TCCCTCATC CCAGTCTGA TGGCCGTTG GTGAGTGTCT GGTGCCCTGG
5601 TGGCTGCCCT CAGCTCTCTT CTGGCTTCTC GAGCAGGAAG CGAGCAGAGG
5651 CTCCACAGGC TTACGCTGCT CTCCCTGACAG CCACACGCA CCCTCGGTGC
5701 AGAGTGCAGA GGCAGCTCTG GTTCCCTCCAG CCACCTCAGT CCCTCTTGG
5751 GAGGTGATGT TCCCATTGTT TTTCAAGGC CTCACCTTCA ACTGTCTGT
5801 TTAGAATTCC CCTCTGGAGG GCTATGGCCT CCCTATGCTT TCACTTCCA
5851 CCTCTCTACC TAAGTTCTT CCCAGCACAT CGCCAGCCCT GGGCTGGGG
5901 ATGCCCCAA TGCTGTACCT GGCTGACCCC GGATTAAGG CCTCATCCAC
5951 GACCGTGTCC ATCTGCTCTG CCAGCTCTCC CTCCCATCCC CCCACCCCAT
6001 GTCCGCTCC CCACGGCGCC CATCCACAGT GGGACAGAA GGAAGTGAGC
6051 ACACGGCACA CCCGCTGTTG GATTGGTTGC TATTTCTCCC GTCCACAGG
6101 GCCTGACCTG GCCCAGGGTG GGGTGGGGG CTCTGGGAC AGGACATGCA
6151 GGGAGGAAGG GGGGGCGAGG ATTTCCTGT GTTTTATCCA TTTGCAAGTT

FIGURE 3B

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6201 GGTCAACCAAT AGAAATGGGA CTCTGAGGGC TAACAGAAAT GGGACTCTGA
 6251 GGGCTAACAG GAGAGGGCGG CCTGGCTCTG GGCCCCAGCC AGGCCCGAG
 6301 AGTCCTGTCC CCTCTGAGAA GGGGAGGGAG AGAGCTCTAG AAACCAACGG
 6351 AGAAACAGAG AAGGGGGCAG GGGCTCATGT CAGCAAACAC GGCTACATCA
 6401 CGTGACACGC CAGTGACACA GAAACACACG CCAACGCACA CGGCTGCACA
 6451 GCGGGCAGGG GCGGTTAGGG GAAAGGGAGC CGGGGCCACC CATCTGTCC
 6501 TCTGCAGGGC GGGCTGGGG GCAGGGTGAA TGCATAGAAC ACATCATGTG
 6551 TACACGCTCA GGGCGTGGCA AGAGCGTGGC TCGACCCACG GGTACATGGG
 6601 ATGGACACGC AGTGTGCTTC ATGAGGGGTG GGAACAGGGA GGAGGGGAA
 6651 GAGGAAGCAC TGAGCCCTGG CCAGGCCCCG GACCACCCGC AGGGCACACG
 6701 TGGGGCACAT GTGGGCTCAA TGGTTGCAGG CGCCTGGCA GGTAGCACAC
 6751 ATTTGTCCAA GAACATGCAA AAGACACAG CCTCCAGACA ACATGCCAGG
 6801 ACGCACACAG ACAGCAGCCA ACAAGCAGGC ACATCATAGG ATGTGGAGA
 6851 CGCATAGAAA GGGCACAGCA GACCCTTAGA GATCCCCCTGG TCCACCTGAG
 6901 GCCCAGAGAT GGGCAGCTGT GGGCCAATG CCACTCCAGG TGGGGGAGT
 6951 GGTGCCCCAG CCACGCTTCA ACCCTTCTCC TGTGGCCCA AGGCCGTGGG
 7001 ACTTCCGGAA ACACCTGGC TGAATGGGG TCCCTGTCCAG GCGGGCGGAA
 7051 GAGGGGACTG GGGGCTGGGG CCTGCTCTGA TGTCTCCCA GCAGGGCGAG
 7101 ATGGGAGCAG GAGGGCCGTG GCCAGACTTG GGGCAGACTT CCTGCTCTGC
 7151 AGAGGGGCGT TCTGGGAAGG GACAGGCAGG CCCCCAGCTC AGGACAGCCC
 7201 ACCTGGGGTT ACGCACGTGG CCACACTGAC ACACACACAG GACAAGGGAG
 7251 AGCTCGGCTG TCTGAGCTCG GGTAGAGGTG GAGGGGTACT GTGTTCTGGG
 7301 A

(SEQ ID NO: 3)

FEATURES:

Start: 2462
 Exon: 2462-2627
 Intron: 2628-3225
 Exon: 3226-3334
 Intron: 3335-3407
 Exon: 3408-3507
 Intron: 3508-3642
 Exon: 3643-3805
 Intron: 3806-4570
 Exon: 4571-4983
 Stop: 4984

SNPs:

DNA				Protein			
Position	Major	Minor	Domain	Position	Major	Minor	
1010	A	G	Beyond ORF(5')				
1151	C	T	Beyond ORF(5')				
4805	G	A	Exon	258	R	Q	
6293	G	A	Beyond ORF(3')				

Context:

DNA Position

1010 TCCAAGCAGCCCATTGGCGTGGACGAGGAGATCACCTACGACTACAAGTTCCCACTGGAA
 GACAACAAGATCCCGTGTCTGTGTGGCACAGAGAGCTGCCGGGGCTCCCTAACTGAGGT
 GGGGCAAGGATGGGTGCCACACCCCTATTATTCCCCCTGGTGCCCTGAGCTCCAGCAC
 CCCCCCAGCTTAGTGGGCTCAGCAGGGCCCACATGCCCTCATCTCAAGCGTGGGGTTG
 GGGGCCCCAAGCCCAGCGAGGGAGCCTCAGTCCCTGGAGGCAGCTCTGCCCTCCTGTC
 [A;G]
 CCCCTGCCACACCCCCCTGATTGTTTCTTGTGGAGAAGAAGCTGTAAATGTTTGT
 AGCAGCCAGCAGCTGTGTTCTGTGAAACCTGGGTGCCGGCTGTACAGATTCTGTCT

FIGURE 3C

Docket No. CL001181DIV2
Serial No. To Be Assigned
Inventors: Ming-Hui WEI et al.
Title: ISOLATED HUMAN ENZYME PROTEINS...

GGGGGGCTACACAGTCTCTCGCTTGTAAATGGGGACTTCCCTTACGCCCTGCGTG
TACCCCTCCCCAGTTAGGGGCTCTGGGGCAGTGGCCATGTTCTCCCTGGGGGGCT
CTGCACCCCCAGTCTGGGACTCCGTGCTGGAACCCCTGCCATCTGTTCTGCCAGA

1151 CCCCTATTTATCCTGGTGCCTGAGCTCCAGCACCCCCCAGCCTAGTGGGCTC
AGCAGGGCCCACATGCCCATCTCAAGCGTGGGGTGGGGCCCAAGCCAGCGAGG
GAGCCTCAGTCCCCTGGAGGGAGCTTCTGCTCTCTGCCCCCTGCCACCCCCCTG
ATTGTTTTCTTGCAGAGAAGCTGAAATGTTGTAGCAGCCAGCAGCTGTTCC
TGTGGAAACCTGGGTGCCGGCTGTACAGATTCTGCTCTGGGGCTACACAGTCCCT
[C, T]
GCTTTGTGTTAAATGGGACTTCCCTTACGCCCTGCGTGACCCCTCCCCAGTTAGGG
TCTCTGGGAGTGGCCATGTTCTCCCTGGGGGCTCTGACCCCCCAGTCCCTGGGG
CTCCGTGCCCTGGAACCCCTGCCATCTGTTCTGCCAGACCCCTGAGGGTCACTTCC
CTGGGTGCACTCCCCGGCTAGCCAGGGCAGGATGGCGGGTGGTCCCTTGCTGG
CTGGACTGTACATATGTTAAATAGCGAAACCCGACGCCACATTATAATTGTGATTA

4805 AGCAGCCTCGATGTGGTGTGCAAGGGCACTCAGGGTGTGTCGCCCTCTTCCGCCAC
CGGCAGGCAATGTGCCCTGGATGCACTGCTGGCAGCCGGAGCTGGAGCAGCGGGCAG
CCCTGATGGCGGCCAGGTATACTTCTGCTACGATGGATCACCTACAGGAGCTACGAGG
ATTTCACATGGAGTTCTGGCCCTGCGGACTGCGGCTGGTGGCGCCGCCATTGC
TGCCCTACTGGCTGCTGGTGTCCCTGGCTGCCCTCAATGCCCTGCTGCACTGGCTGCT
[G, A]
GCCACTGGTGTCTACGCACCCCTGCTGAACCCCTACAGCTGCCGTGCCAACACAC
CTTCACCGTCAGCACCGACAAGGCTCAGGCCATTCCGCTATGAGCCCTGTTCTG
GGAGGATAGCGGACCCGACCATCTGGGTACAGGCCCTACGGGTTCAAGCCAGTG
ACGGTGGGCTGGGCTGGAGGGCCAGATACAGCACATCCACCCAGGTCCCAGCCCTC
ACACCCCTGGACGGGAAGGGACAGCTGCAATTCCAGAGCAGGAGGAGGCTTCTGGGCCA

6293 CACCCATGTCCGCCCTCCCCACGGGCCCATCCACGTGGGACAGAAGGAAGTGA
ACGGCACACCCGCTGTTGGATGGTTGCTATTTCTCCGCTCCACAGGGCTGACCTGG
CCAGGGTGGGGTGGGGGCTCTGGGACAGGACATGCAAGGGAGGAAGGGGGGGCAGGAT
TTTCTGTTTATCCATTGCAAGTTGGTCACCAATAGAAATGGACTCTGAGGGCTA
ACAGAAATGGGACTCTGAGGGCTAACAGGAGAGGGCCCTGGCTCTGGGCCAGCCAG
[G, A]
CCCCAGGAGTCTGCTCCCTCTGAGAAGGGAGGGAGAGAGCTCTAGAAACCAACGGAGA
AACAGAGAAGGGGGCAGGGCTCATGTCAGCAAACACGGCTACATCAGTGAACGCCAG
TGACACAGAAACACGCCAACGCAACGGCTCACAGCGGGCAGGGCGGTTAGGGGAA
AGGGAGGCCGGGCCACCCATCTGCTCTGCAAGGGGGCTGGGGCAGGGTGAATGC
ATAGAACACATCATGTTACACGCTCAGGGCTGGCAAGAGCGTGCACCCACGGG

Chromosome map:
Chromosome 12

FIGURE 3D